

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Dulac, Catherine
Axel, Richard

(ii) TITLE OF INVENTION: Cloning Of Vertebrate Pheromone
Receptors And Uses Thereof

(iii) NUMBER OF SEQUENCES: 18

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: White, John P.
(B) REGISTRATION NUMBER: 28678
(C) REFERENCE/DOCKET NUMBER: 48557

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAACATAAGT CCAGTTATCT ACAGGTACAG GTTGATGAGA GGCCTCTCCA TTTCCACCA	60
CTGCCTGTTG AGTGTCCCTCC AGGCCATCAA CCTCACCCCCA AGGAGCTCCC GTTTGGCAAT	120
GTTCAGAGAT CCTCACATCA CAAACCGCGT TGCTTCTCT TGCTGTGGGT CTTCCACATA	180
TCCATTAGTG GAAGCTTCTT AGTCTCCACT CTTCCCTCCA AAAATGTTGC CTCAAATAGT	240
GTTACATTG TCACTCAATC CTGCTCTGCT GGGCCCTGA GTTGCTTCCT TGGGCAGACA	300
ATTTTCACAC TGATGACATT TCAGGATGTC TCCTTGCAGC TCATGGCCCC CTTCAGTGGA	360
TACATGGTGA TTCTCTTGTG CAGGCATAAC AGGCAGTCTC AGCATCTTCA TAGTATCAAC	420
CTTTCTCCAA AAGCACCCCC AGATAAAAGG GCCATCCAGA GCATTCTTT GCTCGTGAGT	480
TTCTTTGTGT TCATGTGCCT TTTCCCATTT GCTGCCTTAA CACTTCTGTC	530

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTTCGGCACG AGTCACCTG CCCTCGAATT TCAATTGAG TAAGTGACCA GCAATGGAGT 60
ACAGAACATCAG AAGATGGTTG GATCCCAGGC AGGCTGTGGG AGGAGGAACT CTGGAACCTGC 120
ATGAGGAGTT TGAGCACCTG CCATGGAGTA GCTGATCTCT GAGGACCCCT CACACAGGTC 180
CTGTGTTCTA CATCAAGTGC ATATTTTCC TAGGATATTTC ATTTCCGTAA GTCCTGAAAT 240
TACTTAATTT TTATAGGAGT TCTCATATAT GATGAATAAG AACAGCAGAC TCTACACTGA 300
TTCTAACATA AGGAATACCT TTTTCGCTGA AATTGGCATT GGAGTCTCAG CCAATAGCCT 360
CCTACTTCTC TTCAACATCT TCAAGTTAAT TTGTGGCAG AGGTCCAGAC TCACTGACCT 420
GCCCATGGT CTCTTGTCCC TAATCAACTT ACTTATGCTA CTGATGACGG CATTCACTAGC 480
CACAGACACT TTTATTTCTT GGAGAGGGTG GGATGACATC ATATGTAAAT CCCTTCTCTA 540
CCTGTACAGA ACTTTTAGAG GTCTCTCTCT TTGTACCAGC TGCCTGTTGA GTGTCCTGCA 600
GGCCATCATC CTCAGTCCC GAAGCTCCTG TTTAGCAAAG TTCAAACATA AGCCTTCCCA 660
TCACATCTCC TGTGCCATTCTC TTTCTCTGAG TGTCTCTAC ATGTTCACTA GCAGTCACCT 720
CTTAGTATCC ATCATTGCCA CCCCCAAATT GACCACGAAT GACTTTATTTC ATGTTACTCA 780
GTGGTGCTCT ATTCTACCCA TGAGTTACCT CATGCAAAGC ATGTTTCTA CACTGCTGGC 840
CATCAGGGAT GTCTTTCTTA TTAGTCTCAT GGTCTGTCA ACATGGTACA TGGTGGCTCT 900
CTTGTGTAGG CACAGGAAAC AGACCCGGCA TCTTCAGGGT ACCAGCCTTT CCCCCAAAAGC 960
ATCCCCAGAA CAAAGGGCCA CCCGTTCCAT CCTGATGCTC ATGAGCTTAT TTGTTCTGAT 1020

GTCTGTCTTT GACAGCATTG TCTGCAGCTC AAGAACTATG TATCTGAATG ATCCAATATC	1080
TTATTCTTAT CAACTATTTA TGGTGCACAT CTATGCCACA GTAAGCCCTT TTGTGTTTAT	1140
TGTCACTGAA AAACATATAG TTAACTCTTT GAGGTCCATG TGTGTGAAGG TGCATGAATG	1200
TTTGAATATT CCTTGATAGC AAGCTCCATT AAGAGGAGCC AATGTAAGCA TCAGAACTGT	1260
CAATCATGGC GTGCTATGTG CTTTGGCATA TGTGAAATAT GAAGTTGTTT TTCTGTTAAA	1320
ATGATTTACT TTAACTGACG AGATGATGAA CGTAACAGAA GATTAAACCA CATCCCCTT	1380
GATAT	1385

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTGGATCCCC CGGGCTGCAG GAATTGGCA CGAGCCGTGA TTAAGGGACT TTGAACCTTT	60
CAAGGGATTT GGAGTTTAT GAAGAATTG AAGATTACA GAGTTACAG GAATGGAGCT	120
GACCAGCCAC TATGACATGC CTTATATCTC CAAGAGCATA AATATAAGGC ATGGCATGAG	180
AGGACCAGCA GCCACTGTTC TCATATATGA TGAATAAGAA CAGCAGAGTC CACACTGATT	240
CTACCATAAG GAATACCTTC TCCACTGAAA TTGGCATTGG AATCTTAGCC AACAGTTCC	300
TACTTCTCTT CCACATCTTC AAGTTTATTC GTGGACAGAG GTCCAGACTC ACTGACCTGC	360

CCATTGGTCT CTTGTCCCTA ATCCACCTAC TGATGCTACT GATGGGGGCA TTCATAGCCA 420
TAGACATTT TATTTCTTGG AGGGGATGGG ATGACATCAT ATGTAATTC CTTGTCTACT 480
TGTACAGAAG TTTTAGAGGT CTCTCTTT GTACCACCTG CATGTTGAGT GTCCTGCAGG 540
CCATCACCCCT CAGCCCCAGA AGCTCCTGTT TAGCAAAGTT CAAACATAAG TCTCCCCATC 600
ACGTCTCCTG TGCCATTATT TCGCTGAGCA TCCTCTACAT GTTCATTAGC AGTCACCTCT 660
TAGTATCCAT CAATGCCACC CCCAATTGGA CCACGAACAA CTTTATGCAA GTTACTCAGT 720
CCTGCTACAT TATAACCCTTG AGTTACCTCA TGCAAAGCAT GTTTTCTACA CTTCTGGCCA 780
TCAGAGATAT CTCTCTTATT AGTCTCATGG TCCTCTCGAC TTGTTACATG GAGGTTCTCT 840
TGTGTAGGCA CAGGAATCAG ATCCAGCATC TTCAAGGGAC CAACCTTTCC CCAAAAGCAT 900
CTCCAGAACAA AAGGGCCACA CAGACCATCC TGATGCTCAT GACCTTCTTT GTCCTAATGT 960
CCATTTCGA CAGCATTGTC TCCTGTTCAA GAACTATGTA TCTGAATGAT CCAACATCTT 1020
ACTATATTCA AATATTTGTA GTGGACATCT ATGCCACAGT CAGCCCTTT GTGTTTATGA 1080
GCACTGGAAA ACATATAGTT AACTTTGTA AGTCCATGTG TGTGAGGGTG AAGAATGTTT 1140
GAATATTCA TAATGGACAA GATCCTTAA GAGGAGCCAA TGTAGTCATC AGAACTGTCA 1200
GTCATGGTGT GCTGTCTATG TGCTTGGTA AATGTGAATC ATGAAGTTGT TTTCTGGTA 1260
AAATGATTAA CTTAACCAA CTCATGATTG TAAACATGTA ACAGGAGATT AAACAATATC 1320
CCCTTCGGAA A 1331

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AATTGGCAC GAGCAAAGGC AGGGAAGATG CTCCACTGGG ATGTCATGTC TCTATGCTCC 60
ACAGTGGAAA AGTTGTCACA TTGTACAAAC ACTAAAATTA CGAATTGCTC ACAGGCACTA 120
AAAGCTTCCT TAATCCTGTG CAGGATCTCC TCAGGTACAG AGTCCTCCTG ATACGTCTAT 180
CTGGTCAGAG GAAAGAGCTG ATCAGTCATT AACAGAGCTG ATTTGGTCCC TCCAAGGTCA 240
CATGACAAGG ACTGTATGAG AAAACCAGCA GTGACATGTC TATAGAGATC ATTCTGTGCC 300
ACACCCAGCT CCATGTTTGG TTTGTGGTAT TTGCTTCCTA TCCACATACA ATGAATAAAG 360
ACAACACACT CCATGTTGAC ACAATCATGA AAATCACTAT GTTCTCTGAA GTGAGTGGT 420
GCATCTTAGC TAACAGTATC CTGTTTTTG GTCACCTGTG CATGCTCCTT GGAGAGAAC 480
AGCCTAAGCC CATTCACTTC TACATTGCAT CCTTGTCCCT AACACAACTA ATGCTGCTTA 540
TAACTATGGG ACTCATAGCT GCTGACATGT TTATTTCTCA GGGGATATGG GATTCTACCT 600
CATGCCAGTC CCTTATCTAT TTGCACAGGC TTTCGAGGGG TTTTACCCCTT AGTGCTGCCT 660
GTCTGCTGAA TGTCTTTGG ATGATCACTC TCAGTTCTAA AAAATCCTGT TTAACAAAGT 720
TTAAACATAA CTCTCCCCAT CACATCTCAG GTGCCTTCT TCTCCTCTGT GTTCTCTACA 780
TGTGTTTAG CAGTCACCTT ATTTTATCGA TTATTGCTAC CCCTAACTTG ACCTCAGATA 840
ATTTTATGTA TGTTACTAAG TCCTGTTCAT TTCTACCCAT GTGTTACTCC AGAACAAAGCA 900
TGTTTCCAC AACAAATTGCT GTCAGGGAAAG CCTTTTTAT CGGTCTCATG GCCCTGTCCA 960
GTGGGTACCT GGTGGCTTTC CTCTGGAGAC ACAGGAAGCA GGCCCAGCAT CTTCACAGCA 1020

CCGGCCTTTC TTCAAAGTCA TCTCCAGAGC AAAGGGCCAC CGAGACCATC CTGCTGCTTA	1080
TGAGTTTCTT TGTGGTTCTC TACATTGAA AAAATGTTGT CTTCTACTCA AGGATGAAGT	1140
TCAAGGATGG GTCAACATTC TACTGTGTCC AAATTATTGT GTCCCATAGC TATGCCACTG	1200
TCAGCTCTTT TGTGTTTATT TTCAGTGAAA AGCGTATGAC TAAGATATTG AGGTCAGTGT	1260
GTGCCAGAAT AATAAATAAT TGATTATTCA GTGATGGTA TTGCCCTTA GAATAAACCA	1320
TTACGTTGTC ATCAGAGGTT TGGGTCACTGA CATAATTGGG ACATTCTCTG TCTTAAATTG	1380
ATAAATGAAA TTTCTTTT TCCTGTTAAA ACTGTTTCCT TTGTGTGTGG ATGCCAATA	1440
TATGAAAGAA AACTAACAC CATGTCTCT TACATATCCA ACCAAAAAAA AAAAAAA	1496

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1053 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTTTCCCA CCTCTTCATG CTCTTGAAA AGAACAGATC TAAGCCCATT GATCTCTACA	60
TTGCTTTCTT ATCCTTAACC CAACTAATGC TGCTTATAAC TATTGGACTT ATAGCTGCAG	120
ACATGTTTAT GTCTCGGGGG AGATGGGATT CTACCACATG CCAGTCCCTT ATCTATTG	180
ACAGGCTTTT GAGGGGTTTT ACCCTTGTC CTACCTGTCT GCTGAATGTC CTTGGACCA	240
TCACTCTCAG TCCTAGAAGC TCCTGTTAA CAACATTAA ACATAAATCT CCCCATCACA	300

TCTCAGGTGC CTTCTTTTC TTCTGTGTT CTCATATATC TTTTGGCAGT CACCTCTTT	360
TATCAACAAT TGCTACCCCC AATTTGACTT CAGATAATT TATGTATGTT ACTAAATCCT	420
GTTCATTTCT ACCCATGAGT TACTCCAGAA CAAGCATGTT TTCCACACCA ATGGCCATCA	480
GGGAAGCCCT TCTTATTGGT CTCATTGCC TGTCAGTGG GTACATGGTT GCTTCCTAT	540
GGAGACACAA GAATCAGGCC CGGCATCTTC ACAGCACCAG CCTTTCTCA AAAGTGTCCC	600
CAGAGCAAAG GGCCACCAGG ACCATCATGA TTCTCATGAG CTTCTTGTG GTTCTCTACA	660
TTTTGGAAAA TGTTGTCTTC TACTCTAGGA TGACATTCAA GGATGGGTCA ATGTTCTACT	720
GTGTCCAAAT TATTGTGTCC CATACTATG CCACCATCAG CCCTTTGTG TTTATTTGCA	780
CAGAAAAGCG TATAATTAAA CTTTGGGGGT CAATGTCTAG CAGAATAGTA AGTATTTGAT	840
TACTCAGTGA TGGATATGGT CCCTTAATAT AAACCAATAT GTTGTCTAA TAACTATGGA	900
TCATGACATA TTGGGGACAT TCTGTGTCTT AAATTTATAA AAAAAATTGT CTTTTTTGT	960
GTTTAATCTG TTTCCCTTGT GTGTGGATGA TAAGTATATA AAGGGAAATT AAACAGCGTG	1020
TCCCCTCAGA TATCCAAAAA AAAAAAAA AAA	1053

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3076 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGCTGCAGG AATTGGCAC GAGTCAGAGT CCTTCCCTGC TATGTGTATC TGGAGCCAGC 60
GACTCTTCTA TGGAGAGCAG CTGTGCAGGC AGGTGGTGGA GCGGAAGAAG GCGTGCTGCT 120
GTGACATCAT CAAGATGCTG CCTAGCCCTG CGTCGCTGCT CTTCTGAGGA AGCAGGAGAC 180
TGACCCCTGT GACAATGACT TGATGAGTCA CTCTGTTGTC TACTTACCCCT AGTTCTTGT 240
CCCATACAAT GAGGAGAATC AGCACACTGT ATGGAGTTGT TGACAAGCAA GCTATATTTT 300
TCTCTGAAGT AGTCATCGGG ATCTCATTCA ACAGTATCCT CTTCCCTTTC CACATCTTTC 360
AGTTCCCTTCT TGAGCGTAGG CTCCGGATCA CTGACCTGAT CATCAGTCTC TTGGCCCTCA 420
TCCACCTTGG GATGCTAACCA GTCATGGAT TCAGAGCTGT TGATATTTT GCATCTCAGA 480
ATGTGTGGAA TGACATCAAA TGCAAATCCC TTGCCCACTT ACACAGACTT TTGAGGGGCC 540
TCTCTCTTTG TGCTACCTGT CTGCTGAGTA TCTTCCAGGC CATCACCCCTT AGCCCCAGAA 600
GCTCCTGTTT AGCAAAGTTC AAATATAAAT CCACACAGCA CAGCCTGTGT TCCCTTCTTG 660
TGCTCTGGC CTTCTACATG TCCTGTGGTA CTCACTACTC CTTCACCATC GTTGCTGACT 720
ACAACCTCTC TTCACGCAGT CTCATATTTG TCACTGAATC CTGCATTATT TTACCCATGG 780
ATTACATCAC CAGGGATTAA TTTTCATAT TGGGGATATT TCGGGATGTG TCCTTCATAG 840
GTCTCATGGC CCTCTCCAGC GGGTACATGG TGGCCCTCTT GTGCAGACAC AGGAAACAGG 900
CCCAGCATCT TCACAGGACC AGCCTTCTC CAAAGCATC CCCAGAGCAA AGGGCCACCA 960
GGACCATCCT GTTGCTCATG AGCTTCTTG TGTTGATGTA CTGCTTGGAC TGCACCATAT 1020
CCGCCTCCAG ACTTATGCAC AACGGTGAAC CAATCCACCA CAGTATTCAG ATGATGGTCT 1080
CCAATAGCTA TGCCACCCTC AGCCCTTGC TGTTAATTGT TACTGAAAAT CGAATTAGTA 1140
GGTTTTGAA GTCCTTGCTA GGAAGGACAG TAGATGCTTA AGTATTGAGG GGAGGCAGGC 1200
CCACTAAAGG AGCCAATATG CTAGCTACTG AATAATGAAT CCTGGCCTAG TCCTCATGCA 1260

ATCCTGAACA AATTAATACA TGACTCATGC TTGTTAAC CTGCTTCTTT TGAAATGTGT	1320
ATTACCAACA CCTGTAGATA TTTGAGTCAA ATTTCTTCAT GTGTATTTCT TCTCAGTGTC	1380
AGTAGGGGAC ATCTGTGACA CTTTCACAGA TTAGGGTAAC TTGTGCACTT ATCAATAAGC	1440
TAAAGTGTAC AGCACATTT ACTAAGCCAA TTATCTCAAC AGTTGTTTT CTACCCAATT	1500
AAATATGTAA ATGTTACAC CAAAAAAA AAAAAAAA	1538

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTGGGGTAAA ACGGCTCGAT GACTTCCACA TGTTTGCCA TGGCAGAAC TGCTCCATGC	60
GGGACAAGAA AATCTCTTT CTGGTCTGAC GGGCTTACTG CTGAATTACAC TGTCGGCGAA	120
GGTAAGTTGA TGACTCATGA TGAACCCTGT TCTATGGCTC CAGATGACAA ACATGATCTC	180
ATATCAGGGA CTTGTTCGCA CCTTCCCTAA CAGTATCCTG TTTTTGCCC ACCTCTGCAT	240
GTTCTTGAA GAGAACAGGT CTAAGCCCCT TGATCTGTGC ATTGCTTTCT TATCCTTAAC	300
CCAACTAATG CTGCTTGAA CTATGGACT CATAGCTGCA GACATGTTA TGGCTCAGGG	360
GATATGGGAT ATTACCACAT GCAGGTCCT TATCTATTTT CACAGACTTT TGAGGGTTT	420
CAACCTTGT GCTGCCTGTC TACTGCATAT CCTTTGGACC TTCACTCTCA GTCCTAGAAG	480

CTCCTGTTA ACAAGTTA AACATAAATC TCCCCATCAC ATCTCAGGTG CCTATCTTT	540
CTTCTGTGTT CTCTATATGT CCTTTAGCAG TCACCTCTT GTATTGGTCA TTGCTACCTC	600
CAATTAAACC TCAGATCATT TTATGTATGT TACTCAGTCC TGCTCACTTC TACCCATGAG	660
TTACTCCAGA ACAAGCACGT TTTCTTACT GATGGTCACC AGGAAAGTCT TTCTTATCAG	720
TCTCATGGCC CTGTCCAGTG GGTACATGGT GACTCTCTA TGGAGGCACA AGAAGCAGGC	780
CCAGCATCTT CACAGCACCA GACTTCTTC AAAAGCATCC CCACAGCAAA GGGCCACCAG	840
GACCATCCTG CTGCTTATGA CCTTCTTGT GGTTTCTAC ATTTAGGCA CTGTTATCTT	900
CCACTCAAGG ACTAAGTTCA AGGATGGTC AATCTTCTAC TGTGTCCAAA TTATTGTGTC	960
CCATAGCTAT GCCACTATCA GCCCATTGT GTTGTAAAAAAGC GCATAATCAA	1020
GTTTTTTAGA TCAATGTGTG GCAGAATAGT AAATACTTGA TTATTCAGT ATGAGTATGG	1080
GTCATGAATA TAGTCTAGTA AATTGTGATC AGAGTTATGG CTCATGACAT ATTAAAAACA	1140
TTCTCTAATT TAAGTTAAC ATATAAAATT ATCTTATTTC TCTTAAATGT GTTTACTTTG	1200
TGTGTATTAA AAGTATGTAA AAGATAATTA ATCCCCAAAT ACACCTTTT TTCAAATTAA	1260
AAAAA	1264

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Met Asn Lys Asn Ser Arg Leu Tyr Thr Asp Ser Asn Ile Arg Asn
1 5 10 15

Thr Phe Phe Ala Glu Ile Gly Ile Gly Val Ser Ala Asn Ser Leu Leu
20 25 30

Leu Leu Phe Asn Ile Phe Lys Leu Ile Cys Gly Gln Arg Ser Arg Leu
35 40 45

Thr Asp Leu Pro Ile Gly Leu Leu Ser Leu Ile Asn Leu Leu Met Leu
50 55 60

Leu Met Thr Ala Phe Ile Ala Thr Asp Thr Phe Ile Ser Trp Arg Gly
65 70 75 80

Trp Asp Asp Ile Ile Cys Lys Ser Leu Leu Tyr Leu Tyr Arg Thr Phe
85 90 95

Arg Gly Leu Ser Leu Cys Thr Ser Cys Leu Leu Ser Val Leu Gln Ala
100 105 110

Ile Ile Leu Ser Pro Arg Ser Ser Cys Leu Ala Lys Phe Lys His Lys
115 120 125

Pro Ser His His Ile Ser Cys Ala Ile Leu Ser Leu Ser Val Leu Tyr
130 135 140

Met Phe Ile Ser Ser His Leu Leu Val Ser Ile Ile Ala Thr Pro Asn
145 150 155 160

Leu Thr Thr Asn Asp Phe Ile His Val Thr Gln Trp Cys Ser Ile Leu
165 170 175

Pro Met Ser Tyr Leu Met Gln Ser Met Phe Ser Thr Leu Leu Ala Ile
180 185 190

Arg Asp Val Phe Leu Ile Ser Leu Met Val Leu Ser Thr Trp Tyr Met
195 200 205

DRAFT 4/20/2000

Val Ala Leu Leu Cys Arg His	Arg Lys Gln Thr Arg His	Leu Gln Gly	
210	215	220	
Thr Ser Leu Ser Pro Lys Ala Ser Pro Glu Gln Arg Ala Thr Arg Ser			
225	230	235	240
Ile Leu Met Leu Met Ser Leu Phe Val Leu Met Ser Val Phe Asp Ser			
245	250	255	
Ile Val Cys Ser Ser Arg Thr Met Tyr Leu Asn Asp Pro Ile Ser Tyr			
260	265	270	
Ser Tyr Gln Leu Phe Met Val His Ile Tyr Ala Thr Val Ser Pro Phe			
275	280	285	
Val Phe Ile Val Thr Glu Lys His Ile Val Asn Ser Leu Arg Ser Met			
290	295	300	
Cys Val Lys Val His Glu Cys Leu Asn Ile Pro			
305	310	315	

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Met Met Asn Lys Asn Ser Arg Leu His Ile Asp Ser Asn Ile Arg Asn
1 5 10 15

Thr Phe Phe Thr Glu Ile Gly Ile Gly Val Ser Ala Asn Ser Leu Leu
20 25 30

Leu Leu Phe Asn Ile Phe Lys Phe Ile His Gly Gln Arg Ser Arg Leu
35 40 45

Thr Asp Leu Pro Ile Gly Leu Leu Ser Leu Ile Asn Leu Leu Met Leu
50 55 60

Leu Ile Met Ala Cys Ile Ala Thr Asp Ile Phe Ile Ser Cys Arg Arg
65 70 75 80

Trp Asp Asp Ile Ile Cys Lys Ser Leu Leu Tyr Leu Tyr Arg Thr Phe
85 90 95

Arg Gly Leu Ser Leu Ser Thr Thr Cys Leu Leu Ser Val Leu Gln Ala
100 105 110

Ile Ile Leu Ser Pro Arg Ser Ser Cys Leu Ala Lys Tyr Lys His Lys
115 120 125

Pro Pro His His Ile Phe Cys Ala Met Leu Phe Leu Ser Val Leu Tyr
130 135 140

Met Phe Ile Ser Ser His Leu Leu Leu Ser Ile Ile Ala Thr Pro Asn
145 150 155 160

Leu Thr Thr Asn Asp Phe Ile His Val Ser Gln Ser Cys Ser Ile Leu
165 170 175

Pro Met Ser Tyr Leu Met Gln Ser Met Phe Ser Thr Leu Leu Ala Ile
180 185 190

Arg Asn Val Phe Leu Ile Ser Leu Ile Val Leu Ser Thr Trp Tyr Met
195 200 205

Val Ala Leu Leu Cys Arg His Arg Lys Gln Thr Arg His Leu Gln Asp
210 215 220

Thr Ser Leu Ser Arg Lys Ala Ser Pro Glu Gln Arg Ala Thr Arg Ser
225 230 235 240

Ile Leu Met Leu Arg Ser Leu Phe Gly Leu Met Ser Ile Phe Asp Ser
245 250 255

Ile Ala Ser Cys Ser Arg Thr Met Tyr Leu Asn Asp Pro Thr Ser Tyr
260 265 270

Ser Ile Gln Leu Leu Val Val His Ile Tyr Ala Thr Val Ser Pro Phe
275 280 285

Val Phe Met Ile Thr Glu Lys His Ile Val Asn Tyr Leu Lys Ser Met
290 295 300

Tyr Val Arg Val Leu Asn Val
305 310

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Met Asn Lys Asn Ser Arg Val His Thr Asp Ser Thr Ile Arg Asn
1 5 10 15

Thr Phe Ser Thr Glu Ile Gly Ile Gly Ile Leu Ala Asn Ser Phe Leu
20 25 30

Leu Leu Phe His Ile Phe Lys Phe Ile Arg Gly Gln Arg Ser Asp Leu
35 40 45

Thr Asp Leu Pro Ile Gly Leu Leu Ser Leu Ile His Leu Leu Met Leu
50 55 60

Leu Met Gly Ala Phe Ile Ala Ile Asp Ile Phe Ile Ser Trp Arg Gly
65 70 75 80

Trp Asp Asp Ile Ile Cys Lys Phe Leu Val Tyr Leu Tyr Arg Ser Phe
85 90 95

Arg Gly Leu Ser Leu Cys Thr Thr Cys Met Leu Ser Val Leu Gln Ala
100 105 110

Ile Thr Leu Ser Pro Arg Ser Ser Cys Leu Ala Lys Phe Lys His Lys
115 120 125

Ser Pro His His Val Ser Cys Ala Ile Ile Ser Leu Ser Ile Leu Tyr
130 135 140

Met Phe Ile Ser Ser His Leu Leu Val Ser Ile Asn Ala Thr Pro Asn
145 150 155 160

Leu Thr Thr Asn Asn Phe Met Gln Val Thr Gln Ser Cys Tyr Ile Ile
165 170 175

Pro Leu Ser Tyr Leu Met Gln Ser Met Phe Ser Thr Leu Leu Ala Ile
180 185 190

Arg Asp Ile Ser Leu Ile Ser Leu Met Val Leu Ser Thr Cys Tyr Met
195 200 205

Glu Val Leu Leu Cys Arg His Arg Asn Gln Ile Gln His Leu Gln Gly
210 215 220

Thr Asn Leu Ser Pro Lys Ala Ser Pro Glu Gln Arg Ala Thr Gln Thr
225 230 235 240

Ile Leu Met Leu Met Thr Phe Phe Val Leu Met Ser Ile Phe Asp Ser
245 250 255

Ile Val Ser Cys Ser Arg Thr Met Tyr Leu Asn Asp Pro Thr Ser Tyr
260 265 270

Tyr Ile Gln Ile Phe Gly Val Asp Ile Tyr Ala Thr Val Ser Pro Phe
275 280 285

Val Phe Met Ser Thr Glu Lys His Ile Val Asn Phe Leu Lys Ser Met
290 295 300

Cys Val Arg Val Lys Asn Val
305 310

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Asn Lys Asp Asn Thr Leu His Val Asp Thr Ile Met Lys Ile Thr
1 5 10 15

Met Phe Ser Glu Val Ser Val Gly Ile Leu Ala Asn Ser Ile Leu Phe
20 25 30

Phe Gly His Leu Cys Met Leu Leu Gly Glu Asn Lys Pro Lys Pro Ile
35 40 45

His Leu Tyr Ile Ala Ser Leu Ser Leu Thr Gln Leu Met Leu Leu Ile
50 55 60

Thr Met Gly Leu Ile Ala Ala Asp Met Phe Ile Ser Gln Gly Ile Trp
65 70 75 80

Asp Ser Thr Ser Cys Gln Ser Leu Ile Tyr Leu His Arg Leu Ser Arg
85 90 95

Gly Phe Thr Leu Ser Ala Ala Cys Leu Leu Asn Val Phe Trp Met Ile
100 105 110

Thr Leu Ser Ser Lys Lys Ser Cys Leu Thr Lys Phe Lys His Asn Ser
115 120 125

Pro His His Ile Ser Gly Ala Phe Leu Leu Leu Cys Val Leu Tyr Met
130 135 140

Cys Phe Ser Ser His Leu Ile Leu Ser Ile Ile Ala Thr Pro Asn Leu
145 150 155 160

Thr Ser Asp Asn Phe Met Tyr Val Thr Lys Ser Cys Ser Phe Leu Pro
165 170 175

Met Cys Tyr Ser Arg Thr Ser Met Phe Ser Thr Thr Ile Ala Val Arg
180 185 190

Glu Ala Phe Phe Ile Gly Leu Met Ala Leu Ser Ser Gly Tyr Leu Val
195 200 205

Ala Phe Leu Trp Arg His Arg Lys Gln Ala Gln His Leu His Ser Thr
210 215 220

Gly Leu Ser Ser Lys Ser Ser Pro Glu Gln Arg Ala Thr Glu Thr Ile
225 230 235 240

Leu Leu Leu Met Ser Phe Phe Val Val Leu Tyr Ile Leu Glu Asn Val
245 250 255

Val Phe Tyr Ser Ser Arg Met Phe Lys Asp Gly Ser Thr Phe Tyr Cys
260 265 270

Val Gln Ile Ile Val Ser His Ser Tyr Ala Thr Val Ser Ser Phe Val
275 280 285

Phe Ile Phe Thr Glu Lys Arg Met Thr Lys Ile Leu Arg Ser Val Cys
290 295 300

Ala Arg Ile Ile Asn Asn
305 310

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Phe Ser His Leu Phe Met Leu Phe Glu Lys Asn Arg Ser Lys Pro Ile
1 5 10 15

Asp Leu Tyr Ile Ala Phe Leu Ser Leu Thr Gln Leu Met Leu Leu Ile
20 25 30

Thr Ile Gly Leu Ile Ala Ala Asp Met Phe Met Ser Arg Gly Arg Trp
35 40 45

Asp Ser Thr Thr Cys Gln Ser Leu Ile Tyr Leu Asp Arg Leu Leu Arg
50 55 60

Gly Phe Thr Leu Cys Ala Thr Cys Leu Leu Asn Val Leu Trp Thr Ile
65 70 75 80

Thr Leu Ser Pro Arg Ser Ser Cys Leu Thr Thr Phe Lys His Lys Ser
85 90 95

Pro His His Ile Ser Gly Ala Phe Leu Phe Cys Val Leu Tyr Ile
100 105 110

Ser Phe Gly Ser His Leu Phe Leu Ser Thr Ile Ala Thr Pro Asn Leu
115 120 125

Thr Ser Asp Asn Phe Met Tyr Val Thr Lys Ser Cys Ser Phe Leu Pro
130 135 140

Met Ser Tyr Ser Arg Thr Ser Met Phe Ser Thr Pro Met Ala Ile Arg
145 150 155 160

Glu Ala Leu Leu Ile Gly Leu Ile Gly Leu Ser Ser Gly Tyr Met Val

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165

170

175

Ala Phe Leu Trp Arg His Lys Asn Gln Ala Arg His Leu His Ser Thr
180 185 190

Ser Leu Ser Ser Lys Val Ser Pro Glu Gln Arg Ala Thr Arg Thr Ile
195 200 205

Met Ile Leu Met Ser Phe Phe Val Val Leu Tyr Ile Leu Glu Asn Val
210 215 220

Val Phe Tyr Ser Arg Met Thr Phe Lys Asp Gly Ser Met Phe Tyr Cys
225 230 235 240

Val Gln Ile Ile Val Ser His Ser Tyr Ala Thr Ile Ser Pro Phe Val
245 250 255

Phe Ile Cys Thr Glu Lys Arg Ile Ile Lys Leu Trp Gly Ser Met Ser
260 265 270

Ser Arg Ile Val Ser Ile
275

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Arg Arg Ile Ser Thr Leu Tyr Gly Val Val Asp Lys Gln Ala Ile
1 5 10 15

Phe Phe Ser Glu Val Val Ile Gly Ile Ser Phe Asn Ser Ile Leu Phe
20 25 30

Leu Phe His Ile Phe Gln Phe Leu Leu Glu Arg Arg Leu Arg Ile Thr
35 40 45

Asp Leu Ile Ile Ser Leu Leu Ala Leu Ile His Leu Gly Met Leu Thr
50 55 60

Val Met Gly Phe Arg Ala Val Asp Ile Phe Ala Ser Gln Asn Val Trp
65 70 75 80

Asn Asp Ile Lys Cys Lys Ser Leu Ala His Leu His Arg Leu Leu Arg
85 90 95

Gly Leu Ser Leu Cys Ala Thr Cys Leu Leu Ser Ile Phe Gln Ala Ile
100 105 110

Thr Leu Ser Pro Arg Ser Ser Cys Leu Ala Lys Phe Lys Tyr Lys Ser
115 120 125

Thr Gln His Ser Leu Cys Ser Leu Leu Val Leu Trp Ala Phe Tyr Met
130 135 140

Ser Cys Gly Thr His Tyr Ser Phe Thr Ile Val Ala Asp Tyr Asn Phe
145 150 155 160

Ser Ser Arg Ser Leu Ile Phe Val Thr Glu Ser Cys Ile Ile Leu Pro
165 170 175

Met Asp Tyr Ile Thr Arg His Leu Phe Phe Ile Leu Gly Ile Phe Arg
180 185 190

Asp Val Ser Phe Ile Gly Leu Met Ala Leu Ser Ser Gly Tyr Met Val
195 200 205

Ala Leu Leu Cys Arg His Arg Lys Gln Ala Gln His Leu His Arg Thr
210 215 220

Ser Leu Ser Pro Lys Ala Ser Pro Glu Gln Arg Ala Thr Arg Thr Ile
225 230 235 240

Leu Leu Leu Met Ser Phe Phe Val Leu Met Tyr Cys Leu Asp Cys Thr
245 250 255

Ile Ser Ala Ser Arg Leu Met His Asn Gly Glu Pro Ile His His Ser
260 265 270

Ile Gln Met Met Val Ser Asn Ser Tyr Ala Thr Leu Ser Pro Leu Leu
275 280 285

Leu Ile Val Thr Glu Asn Arg Ile Ser Arg Phe Leu Lys Ser Leu Leu
290 295 300

Gly Arg Thr Val Asp Ala
305 310

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Met Asn Pro Val Leu Trp Leu Gln Met Thr Asn Met Ile Ser Tyr
1 5 10 15

Gln Gly Leu Val Arg Thr Phe Pro Asn Ser Ile Leu Phe Phe Ala His
20 25 30

Leu Cys Met Phe Phe Glu Glu Asn Arg Ser Lys Pro Ile Asp Leu Cys
35 40 45

Ile Ala Phe Leu Ser Leu Thr Gln Leu Met Leu Leu Val Thr Met Gly
50 55 60

Leu Ile Ala Ala Asp Met Phe Met Ala Gln Gly Ile Trp Asp Ile Thr
65 70 75 80

Thr Cys Arg Ser Leu Ile Tyr Phe His Arg Leu Leu Arg Gly Phe Asn
85 90 95

Leu Cys Ala Ala Cys Leu Leu His Ile Leu Trp Thr Phe Thr Leu Ser
100 105 110

Pro Arg Ser Ser Cys Leu Thr Lys Phe Lys His Lys Ser Pro His His
115 120 125

Ile Ser Gly Ala Tyr Leu Phe Phe Cys Val Leu Tyr Met Ser Phe Ser
130 135 140

Ser His Leu Phe Val Leu Val Ile Ala Thr Ser Asn Leu Thr Ser Asp
145 150 155 160

His Phe Met Tyr Val Thr Gln Ser Cys Ser Leu Leu Pro Met Ser Tyr
165 170 175

Ser Arg Thr Ser Thr Phe Ser Leu Leu Met Val Thr Arg Glu Val Phe
180 185 190

Leu Ile Ser Leu Met Ala Leu Ser Ser Gly Tyr Met Val Thr Leu Leu
195 200 205

Trp Arg His Lys Lys Gln Ala Gln His Leu His Ser Thr Arg Leu Ser
210 215 220

Ser Lys Ala Ser Pro Gln Gln Arg Ala Thr Arg Thr Ile Leu Leu Leu
225 230 235 240

Met Thr Phe Phe Val Val Phe Tyr Ile Leu Gly Thr Val Ile Phe His
245 250 255

Ser Arg Thr Lys Phe Lys Asp Gly Ser Ile Phe Tyr Cys Val Gln Ile
260 265 270

Ile Val Ser His Ser Tyr Ala Thr Ile Ser Pro Phe Val Phe Val Phe
275 280 285

Ser Glu Lys Arg Ile Ile Lys Phe Phe Arg Ser Met Cys Gly Arg Ile
290 295 300

Val Asn Thr
305

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asn Ile Ser Pro Val Ile Tyr Arg Tyr Arg Leu Met Arg Gly Leu Ser
1 5 10 15

Ile Ser Thr Thr Cys Leu Leu Ser Val Leu Gln Ala Ile Asn Leu Thr
20 25 30

Pro Arg Ser Ser Arg Leu Ala Arg Ser Ser His His Lys Pro Arg Cys
35 40 45

Phe Leu Leu Leu Trp Val Phe His Ile Ser Ile Ser Gly Ser Phe Leu
50 55 60

Val Ser Thr Leu Pro Ser Lys Asn Val Ala Ser Asn Ser Val Thr Phe
65 70 75 80

Val Thr Gln Ser Cys Ser Ala Gly Pro Leu Ser Cys Phe Leu Gly Gln
85 90 95

Thr Ile Phe Thr Leu Met Thr Phe Gln Asp Val Ser Leu Gln Leu Met
100 105 110

Ala Pro Phe Ser Gly Tyr Met Val Ile Leu Leu Cys Arg His Asn Arg
115 120 125

Gln Ser Gln His Leu His Ser Ile Asn Leu Ser Pro Lys Ala Pro Pro
130 135 140

Asp Lys Arg Ala Ile Gln Ser Ile Leu Leu Val Ser Phe Phe Val
145 150 155 160

Phe Met Cys Leu Phe Pro Phe Ala Ala Leu Thr Leu Leu
165 170

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Lys Arg Lys Lys Ser Phe Leu Leu Cys Ile Gly Trp Leu Ala Leu
1 5 10 15

Thr Asp Leu Val Gly Gln Leu Leu Thr Ser Pro Val Val Ile Leu Val
20 25 30

Tyr Leu Ser Gln Arg Arg Trp Glu Gln Leu Asp Pro Ser Gly Arg Leu
35 40 45

Cys Thr Phe Phe Gly Leu Thr Met Thr Val Phe Gly Leu Ser Ser Leu
50 55 60

Leu Val Ala Ser Ala Met Ala
65 70

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Gly	Gln	Arg	Ser	Arg	Leu	Thr	Asp	Leu	Pro	Ile	Gly	Leu	Leu	Ser	Leu
1															15
Ile Asn Leu Leu Met Leu Leu Ile Met Ala Cys Ile Ala Thr Asp Ile															
														30	
Phe Ile Ser Cys Arg Arg Trp Asp Asp Ile Ile Cys Lys Ser Leu Leu															
														45	
Tyr Leu Tyr Arg Thr Phe Arg Gly Leu Ser Leu Ser Thr Thr Cys Leu															
														60	
Leu Ser Val Leu Gln Ala Ile Ile Leu Ser															
														65	
														70	

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Lys Cys Lys Ser Leu Ala His Leu His Arg Leu Leu Arg Gly Leu Ser
 1 5 10 15
 Leu Cys Ala Thr Cys Leu Leu Ser Ile Phe Gln Ala Ile Thr Leu Ser
 20 25 30
 Pro Arg Ser Ser Cys Leu Ala Lys Ser Thr Gln His Ser Leu Cys Ser
 35 40 45
 Leu Leu Val Leu Trp Ala Phe Tyr Met Ser Cys Gly Thr His Tyr Ser
 50 55 60
 Phe Thr Ile Val Ala Asp Tyr Asn Phe Ser Ser Arg Ser Leu Ile Phe
 65 70 75 80
 Val Thr Glu Ser Cys Ile Ile Leu Pro Met Asp Tyr Ile Thr Arg Asp
 85 90 95
 Leu Phe Phe Ile Leu Gly Ile Phe Arg Asp Val Ser Phe Ile Gly Leu
 100 105 110
 Met Ala Leu Ser Ser Gly Tyr Met Val Ala Leu Leu Cys Arg His Arg
 115 120 125
 Lys Gly Ala Gln His Leu His Arg Thr Ser Leu Ser Pro Lys Ala Ser
 130 135 140
 Pro Glu Gln Arg Ala Thr Arg Thr Ile Leu Leu Leu Met Ser Phe Phe
 145 150 155 160
 Val Leu Met Tyr Cys Leu Asp Cys Thr Ile Ser Ala Ser Arg
 165 170